



## SEQUENCE LISTING

<110> Goodwin, Raymond G.  
Smith, Craig A.

<120> 4-1BB Polypeptides and DNA Encoding 4-1BB Polypeptides

<130> 2801-C

<140> US 08/910,449

<141> 1997-08-05

<150> US 08/236,918

<151> 1994-05-06

<150> US 08/060,843

<151> 1993-05-07

<160> 17

<170> PatentIn version 3.3

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<212> DNA

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<222> (53)..(979)

<223> (Clone: murine 4-1BB-L)

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ggt act tcg tgc ccc tcg gat gcg gcg ctc ctc aga gat acc ggg ctc 154  
Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly Leu  
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ctc gcg gac gct gcg ctc ctc tca gat act gtg cgc ccc aca aat gcc 202  
Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn Ala  
35 40 45 50

gcg ctc ccc acg gat gct gcc tac cct gcg gtt aat gtt cgg gat cgc 250  
Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp Arg  
55 60 65

gag gcc gcg tgg ccg cct gca ctg aac ttc tgt tcc cgc cac cca aag 298  
Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro Lys  
70 75 80

ctc tat ggc cta gtc gct ttg gtt ttg ctg ctt ctg atc gcc gcc tgt 346  
Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala Ala Cys  
85 90 95

gtt cct atc ttc acc cgc acc gag cct cgg cca gcg ctc aca atc acc	394
Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile Thr	
100 105 110	
acc tcg ccc aac ctg ggt acc cga gag aat aat gca gac cag gtc acc	442
Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val Thr	
115 120 125 130	
cct gtt tcc cac att ggc tgc ccc aac act aca caa cag ggc tct cct	490
Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser Pro	
135 140 145	
gtg ttc gcc aag cta ctg gct aaa aac caa gca tcg ttg tgc aat aca	538
Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn Thr	
150 155 160	
act ctg aac tgg cac agc caa gat gga gct ggg agc tca tac cta tct	586
Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu Ser	
165 170 175	
caa ggt ctg agg tac gaa gaa gac aaa aag gag ttg gtg gta gac agt	634
Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp Ser	
180 185 190	
ccc ggg ctc tac tac gta ttt ttg gaa ctg aag ctc agt cca aca ttc	682
Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr Phe	
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Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu Gln	
215 220 225	
gca aag cct cag gta gat gac ttt gac aac ttg gcc ctg aca gtg gaa	778
Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val Glu	
230 235 240	
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Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp Ser	
245 250 255	
caa ctg ttg ctc ctg aag gct ggc cac cgc ctc agt gtg ggt ctg agg	874
Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu Arg	
260 265 270	
gct tat ctg cat gga gcc cag gat gca tac aga gac tgg gag ctg tct	922
Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu Ser	
275 280 285 290	
tat ccc aac acc acc agc ttt gga ctc ttt ctt gtg aaa ccc gac aac	970
Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp Asn	
295 300 305	
cca tgg gaa tgagaactat ccttcttgtg actcctagtt gctaagtcct	1019
Pro Trp Glu	
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taactggact tggatatttat tctgagcata gctcagacaa gactttatat aattcactag	1139

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 Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg  
 50 55 60  
 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His  
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 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala  
 85 90 95  
 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr  
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 115 120 125  
 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly  
 130 135 140  
 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys  
 145 150 155 160  
 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr  
 165 170 175  
 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val  
 180 185 190  
 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro  
 195 200 205  
 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val  
 210 215 220  
 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr  
 225 230 235 240  
 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser  
 245 250 255  
 Trp Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly

260 265 270  
 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu  
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 Asp Asn Pro Trp Glu  
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 <212> DNA  
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 <222> (4)..(765)  
 <223> (clone: human 4-1BB-L (7A)

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 Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu  
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 gtc gcg ggg ctg ctg ctg ctg ctg ctg ctc gct gcc gcc tgc gcc gtc 144  
 Val Ala Gly Leu Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val  
 35 40 45  
 ttc ctc gcc tgc ccc tgg gcc gtg tcc ggg gct cgc gcc tcg ccc ggc 192  
 Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly  
 50 55 60  
 tcc gcg gcc agc ccg aga ctc cgc gag ggt ccc gag ctt tcg ccc gac 240  
 Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp  
 65 70 75  
 gat ccc gcc ggc ctc ttg gac ctg cgg cag ggc atg ttt gcg cag ctg 288  
 Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu  
 80 85 90 95  
 gtg gcc caa aat gtt ctg ctg atc gat ggg ccc ctg agc tgg tac agt 336  
 Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser  
 100 105 110  
 gac cca ggc ctg gca ggc gtg tcc ctg acg ggg ggc ctg agc tac aaa 384  
 Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys  
 115 120 125  
 gag gac acg aag gag ctg gtg gtg gcc aag gct gga gtc tac tat gtc 432  
 Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val  
 130 135 140  
 ttc ttt caa cta gag ctg cgg cgc gtg gtg gcc ggc gag ggc tca ggc 480

Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly		
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Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly		
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gcc	gcc	gcc	ctg	gct	ttg	acc	gtg	gac	ctg	cca	ccc	gcc	tcc	tcc	gag	576	
Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu		
				180					185					190			
gct	cgg	aac	tcg	gcc	ttc	ggc	ttc	cag	ggc	cgc	ttg	ctg	cac	ctg	agt	624	
Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser		
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gcc	ggc	cag	cgc	ctg	ggc	gtc	cat	ctt	cac	act	gag	gcc	agg	gca	cgc	672	
Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg		
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His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg		
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Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu			
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ctcgagtagc	tgggaccaca	gttggtgtgcc	accacacttg	gctaactttt	taattttttt											1545	
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50 55 60  
Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp  
65 70 75 80  
Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val  
85 90 95  
Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp  
100 105 110  
Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu  
115 120 125  
Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe  
130 135 140  
Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser  
145 150 155 160  
Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala  
165 170 175  
Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala  
180 185 190  
Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala  
195 200 205  
Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His  
210 215 220  
Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val  
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 Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln  
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cct ggt act ttc tgc aga aaa tac aat cca gtc tgc aag agc tgc cct 144  
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cca agt acc ttc tcc agc ata ggt gga cag ccg aac tgt aac atc tgc 192  
 Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys  
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 Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr  
 45 50 55

cac aac gcg gag tgt gag tgc att gaa gga ttc cat tgc ttg ggg cca 288  
 His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro  
 60 65 70

cag tgc acc aga tgt gaa aag gac tgc agg cct ggc cag gag cta acg 336  
 Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr  
 75 80 85

aag cag ggt tgc aaa acc tgt agc ttg gga aca ttt aat gac cag aac 384  
 Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn  
 90 95 100 105

ggt act ggc gtc tgt cga ccc tgg acg aac tgc tct cta gac gga agg 432  
 Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg  
 110 115 120

tct gtg ctt aag acc ggg acc acg gag aag gac gtg gtg tgt gga ccc 480  
 Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro  
 125 130 135

cct gtg gtg agc ttc tct ccc agt acc acc att tct gtg act cca gag 528  
 Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu  
 140 145 150

gga gga cca gga ggg cac tcc ttg cag gtc ctt acc ttg ttc ctg gcg 576  
 Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala  
 155 160 165

ctg aca tcg gct ttg ctg ctg gcc ctg atc ttc att act ctc ctg ttc 624

Leu	Thr	Ser	Ala	Leu	Leu	Leu	Ala	Leu	Ile	Phe	Ile	Thr	Leu	Leu	Phe		
170					175					180					185		
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Ser	Val	Leu	Lys	Trp	Ile	Arg	Lys	Lys	Phe	Pro	His	Ile	Phe	Lys	Gln		
				190					195					200			
cca	ttt	aag	aag	acc	act	gga	gca	gct	caa	gag	gaa	gat	gct	tgt	agc	720	
Pro	Phe	Lys	Lys	Thr	Thr	Gly	Ala	Ala	Gln	Glu	Glu	Asp	Ala	Cys	Ser		
			205					210					215				
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Pro	Ser	Thr	Phe	Ser	Ser	Ile	Gly	Gly	Gln	Pro	Asn	Cys	Asn	Ile	Cys		
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Arg	Val	Cys	Ala	Gly	Tyr	Phe	Arg	Phe	Lys	Lys	Phe	Cys	Ser	Ser	Thr		
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Gln	Cys	Thr	Arg	Cys	Glu	Lys	Asp	Cys	Arg	Pro	Gly	Gln	Glu	Leu	Thr		
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Ser	Val	Leu	Lys	Thr	Gly	Thr	Thr	Glu	Lys	Asp	Val	Val	Cys	Gly	Pro		
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Pro	Val	Val	Ser	Phe	Ser	Pro	Ser	Thr	Thr	Ile	Ser	Val	Thr	Pro	Glu		
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Gly	Gly	Pro	Gly	Gly	His	Ser	Leu	Gln	Val	Leu	Thr	Leu	Phe	Leu	Ala		
	155					160					165						
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170					175					180					185		



Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln  
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Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser  
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Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu  
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atg gga aac agc tgt tac aac ata gta gcc act ctg ttg ctg gtc ctc 167  
Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu  
-20 -15 -10  
aac ttt gag agg aca aga tca ttg cag gat cct tgt agt aac tgc cca 215  
Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro  
-5 -1 1 5  
gct ggt aca ttc tgt gat aat aac agg aat cag att tgc agt ccc tgt 263  
Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
10 15 20 25  
cct cca aat agt ttc tcc agc gca ggt gga caa agg acc tgt gac ata 311  
Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
30 35 40  
tgc agg cag tgt aaa ggt gtt ttc agg acc agg aag gag tgt tcc tcc 359  
Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
45 50 55  
acc agc aat gca gag tgt gac tgc act cca ggg ttt cac tgc ctg ggg 407  
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
60 65 70  
gca gga tgc agc atg tgt gaa cag gat tgt aaa caa ggt caa gaa ctg 455  
Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu

75	80	85	
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90	95	100	105
aaa cgt ggc atc tgt	cga ccc tgg aca aac tgt	tct ttg gat gga aag	551
Lys Arg Gly Ile Cys	Arg Pro Trp Thr Asn Cys	Ser Leu Asp Gly Lys	
	110	115	120
tct gtg ctt gtg aat	ggg acg aag gag agg gac	gtg gtc tgt gga cca	599
Ser Val Leu Val Asn	Gly Thr Lys Glu Arg Asp	Val Val Cys Gly Pro	
	125	130	135
tct cca gcc gac ctc	tct ccg gga gca tcc tct	gtg acc ccg cct gcc	647
Ser Pro Ala Asp Leu	Ser Pro Gly Ala Ser Ser	Val Thr Pro Pro Ala	
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cct gcg aga gag cca	gga cac tct ccg cag atc	atc tcc ttc ttt ctt	695
Pro Ala Arg Glu Pro	Gly His Ser Pro Gln Ile	Ile Ser Phe Phe Leu	
	155	160	165
gcg ctg acg tcg act	gcg ttg ctc ttc ctg ctg	ttc ttc ctc acg ctc	743
Ala Leu Thr Ser Thr	Ala Leu Leu Phe Leu Leu	Phe Phe Leu Thr Leu	
	170	175	180
cgt ttc tct gtt gtt	aaa cgg ggc aga aag aaa	ctc ctg tat ata ttc	791
Arg Phe Ser Val Val	Lys Arg Gly Arg Lys Lys	Leu Leu Tyr Ile Phe	
	190	195	200
aaa caa cca ttt atg	aga cca gta caa act act	caa gag gaa gat ggc	839
Lys Gln Pro Phe Met	Arg Pro Val Gln Thr Thr	Gln Glu Glu Asp Gly	
	205	210	215
tgt agc tgc cga ttt	cca gaa gaa gaa gaa gga	gga tgt gaa ctg	884
Cys Ser Cys Arg Phe	Pro Glu Glu Glu Gly Gly	Cys Glu Leu	
	220	225	230
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catccgctat cacagctttc	aaaagcaaga acaccatcct	acataataacc caggattccc	1004
ccaacacacg ttcttttcta	aatgccaatg agttggcctt	taaaaatgca ccactttttt	1064
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gctctctgca gccttgacct	ctgggagctc aagtgatect	cctgcctcag tctcctagta	1184
gctggaacta caaggaaggg	ccaccacacc tgactaactt	ttttgttttt tgtttggtaa	1244
agatggcatt tcgccatggt	gtacaggctg gtctcaaact	cctaggttca ctttggcctc	1304
ccaaagtgct gggattacag	acatgaactg ccaggcccgg	ccaaaataat gcaccacttt	1364
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Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys  
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Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile  
30 35 40

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser  
45 50 55

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly  
60 65 70

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu  
75 80 85

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln  
90 95 100 105

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys  
110 115 120

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro  
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Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala  
140 145 150

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu  
155 160 165

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu  
170 175 180 185

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe  
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Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly  
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tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc	97
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu	
20 25 30	
ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc	145
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	
35 40 45	
ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg	193
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	
50 55 60	
agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg	241
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val	
65 70 75 80	
gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc	289
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	
85 90 95	
acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg	337
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	
100 105 110	
aat ggc aag gac tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc	385
Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala	
115 120 125	
ccc atg cag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca	433
Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro	
130 135 140	
cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag	481
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln	
145 150 155 160	
gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agg cac atc gcc	529
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala	
165 170 175	
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Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr	
180 185 190	
cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc	625
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu	
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acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc	673
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser	
210 215 220	
gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc	721
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser	
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 Leu Ser Pro Gly Lys  
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745

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Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
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Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
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			100					105					110		
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145					150					155					160
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	Ala
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Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
		180						185					190		
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
		195					200					205			
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
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Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
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Leu	Ser	Pro	Gly	Lys											
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